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1012

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RAW SEQUENCE LISTING

DATE: 11/27/2001

PATENT APPLICATION: US/09/922,600

TIME: 13:46:09

Input Set : A:\09922600.raw.txt

Output Set: N:\CRF3\11212001\I922600.raw

PS

1 <110> APPLICANT: Goodman, Corey
 2 Kid, Thomas
 3 Brose, Katja
 4 Tessier-Lavigne, Marc
 5 <120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions
 6 <130> FILE REFERENCE: B98-031-3
 7 <140> CURRENT APPLICATION NUMBER: 09/922,600
 8 <141> CURRENT FILING DATE: 2001-08-03
 9 <150> PRIOR APPLICATION NUMBER: US/09/540,245
 10 <151> PRIOR FILING DATE: 2000-03-31
 11 <150> PRIOR APPLICATION NUMBER: 60/065,544
 12 <151> PRIOR FILING DATE: 1997-11-14
 13 <150> PRIOR APPLICATION NUMBER: 60/081,057
 14 <151> PRIOR FILING DATE: 1998-04-07
 15 <160> NUMBER OF SEQ ID NOS: 20
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 4758
 20 <212> TYPE: DNA
 21 <213> ORGANISM: human
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(4755)
 25 <400> SEQUENCE: 1

26	atg cgc ggc gtt ggc tgg cag atg ctg tcc ctg tcg ctg ggg tta gtg	48
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28	1 5 10 15	
29	ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc	96
30	Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys	
31	20 25 30	
32	tct tgc tcg ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc	144
33	Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser	
34	35 40 45	
35	gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga	192
36	Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly	
37	50 55 60	
38	aat aac atc aca aga att acg aag aca gat ttt gct ggt ctt aga cat	240
39	Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His	
40	65 70 75 80	
41	cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga	288
42	Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg	
43	85 90 95	
44	gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga	336
45	Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg	
46	100 105 110	
47	aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag	384
48	Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys	

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49		115		120		125											
50	cta	tac	agg	ctt	gat	ctc	agt	gaa	aac	caa	att	cag	gca	atc	cca	agg	432
51	Leu	Tyr	Arg	Leu	Asp	Leu	Ser	Glu	Asn	Gln	Ile	Gln	Ala	Ile	Pro	Arg	
52		130					135					140					
53	aaa	gct	ttc	cgt	ggg	gca	gtt	gac	ata	aaa	aat	ttg	caa	ctg	gat	tac	480
54	Lys	Ala	Phe	Arg	Gly	Ala	Val	Asp	Ile	Lys	Asn	Leu	Gln	Leu	Asp	Tyr	
55		145				150					155				160		
56	aac	cag	atc	agc	tgt	att	gaa	gat	ggg	gca	ttc	agg	gct	ctc	cgg	gac	528
57	Asn	Gln	Ile	Ser	Cys	Ile	Glu	Asp	Gly	Ala	Phe	Arg	Ala	Leu	Arg	Asp	
58				165						170				175			
59	ctg	gaa	gtg	ctc	act	ctc	aac	aat	aac	aac	att	act	aga	ctt	tct	gtg	576
60	Leu	Glu	Val	Leu	Thr	Leu	Asn	Asn	Asn	Asn	Ile	Thr	Arg	Leu	Ser	Val	
61			180						185					190			
62	gca	agt	ttc	aac	cat	atg	cct	aaa	ctt	agg	act	ttt	cga	ctg	cat	tca	624
63	Ala	Ser	Phe	Asn	His	Met	Pro	Lys	Leu	Arg	Thr	Phe	Arg	Leu	His	Ser	
64			195				200					205					
65	aac	aac	ctg	tat	tgt	gac	tgc	cac	ctg	gcc	tgg	ctc	tcc	gac	tgg	ctt	672
66	Asn	Asn	Leu	Tyr	Cys	Asp	Cys	His	Leu	Ala	Trp	Leu	Ser	Asp	Trp	Leu	
67		210				215					220						
68	cgc	aaa	agg	cct	cgg	gtt	ggg	ctg	tac	act	cag	tgt	atg	ggc	ccc	tcc	720
69	Arg	Lys	Arg	Pro	Arg	Val	Gly	Leu	Tyr	Thr	Gln	Cys	Met	Gly	Pro	Ser	
70		225			230				235				240				
71	cac	ctg	aga	ggc	cat	aat	gta	gcc	gag	gtt	caa	aaa	cga	gaa	ttt	gtc	768
72	His	Leu	Arg	Gly	His	Asn	Val	Ala	Glu	Val	Gln	Lys	Arg	Glu	Phe	Val	
73			245						250				255				
74	tgc	agt	gat	gag	gaa	gaa	ggg	cac	cag	tca	ttt	atg	gct	cct	tct	tgt	816
75	Cys	Ser	Asp	Glu	Glu	Glu	Gly	His	Gln	Ser	Phe	Met	Ala	Pro	Ser	Cys	
76			260				265					270					
77	agt	gtt	ttg	cac	tgc	cct	gcc	gcc	tgt	acc	tgt	agc	aac	aat	atc	gta	864
78	Ser	Val	Leu	His	Cys	Pro	Ala	Ala	Cys	Thr	Cys	Ser	Asn	Asn	Ile	Val	
79		275				280					285						
80	gac	tgt	cgt	ggg	aaa	ggg	ctc	act	gag	atc	ccc	aca	aat	ctt	cca	gag	912
81	Asp	Cys	Arg	Gly	Lys	Gly	Leu	Thr	Glu	Ile	Pro	Thr	Asn	Leu	Pro	Glu	
82		290				295					300						
83	acc	atc	aca	gaa	ata	cgt	ttg	gaa	cag	aac	aca	atc	aaa	gtc	atc	cct	960
84	Thr	Ile	Thr	Glu	Ile	Arg	Leu	Glu	Gln	Asn	Thr	Ile	Lys	Val	Ile	Pro	
85		305			310				315				320				
86	cct	gga	gct	ttc	tca	cca	tat	aaa	aag	ctt	aga	cga	att	gac	ctg	agc	1008
87	Pro	Gly	Ala	Phe	Ser	Pro	Tyr	Lys	Lys	Leu	Arg	Arg	Ile	Asp	Leu	Ser	
88			325					330				335					
89	aat	aat	cag	atc	tct	gaa	ctt	gca	cca	gat	gct	ttc	caa	gga	cta	cgc	1056
90	Asn	Asn	Gln	Ile	Ser	Glu	Leu	Ala	Pro	Asp	Ala	Phe	Gln	Gly	Leu	Arg	
91			340				345					350					
92	tct	ctg	aat	tca	ctt	gtc	ctc	tat	gga	aat	aaa	atc	aca	gaa	ctc	ccc	1104
93	Ser	Leu	Asn	Ser	Leu	Val	Leu	Tyr	Gly	Asn	Lys	Ile	Thr	Glu	Leu	Pro	
94		355				360					365						
95	aaa	agt	tta	ttt	gaa	gga	ctg	ttt	tcc	tta	cag	ctc	cta	tta	ttg	aat	1152
96	Lys	Ser	Leu	Phe	Glu	Gly	Leu	Phe	Ser	Leu	Gln	Leu	Leu	Leu	Leu	Asn	
97		370				375					380						

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98	gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac	1200
99	Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His	
100	385 390 395 400	
101	aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc	1248
102	Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala	
103	405 410 415	
104	aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc	1296
105	Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala	
106	420 425 430	
107	cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat	1344
108	Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr	
109	435 440 445	
110	ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc	1392
111	Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro	
112	450 455 460	
113	cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc	1440
114	Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe	
115	465 470 475 480	
116	cgt tgt tca ggt aca gaa gat tat cga tca aaa tta agt gga gac tgc	1488
117	Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys	
118	485 490 495	
119	ttt gcg gat ctg gct tgc cct gaa aag tgt cgc tgt gaa gga acc aca	1536
120	Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr	
121	500 505 510	
122	gta gat tgc tct aat caa aag ctc aac aaa atc ccg gag cac att ccc	1584
123	Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro	
124	515 520 525	
125	cag tac act gca gag ttg cgt ctc aat aat aat gaa ttt acc gtg ttg	1632
126	Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu	
127	530 535 540	
128	gaa gcc aca gga atc ttt aag aaa ctt cct caa tta cgt aaa ata aac	1680
129	Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn	
130	545 550 555 560	
131	ttt agc aac aat aag atc aca gat att gag gag gga gca ttt gaa gga	1728
132	Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Gly Ala Phe Glu Gly	
133	565 570 575	
134	gca tct ggt gta aat gaa ata ctt ctt acg agt aat cgt ttg gaa aat	1776
135	Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn	
136	580 585 590	
137	gtg cag cat aag atg ttc aag gga ttg gaa agc ctc aaa act ttg atg	1824
138	Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met	
139	595 600 605	
140	ttg aga agc aat cga ata acc tgt gtg ggg aat gac agt ttc ata gga	1872
141	Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly	
142	610 615 620	
143	ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca	1920
144	Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr	
145	625 630 635 640	
146	gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac	1968

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147	Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn	
148	645 650 655	
149	ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga	2016
150	Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly	
151	660 665 670	
152	gag tgg ctg aga aag aag aga att gtc acg gga aat cct aga tgt caa	2064
153	Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln	
154	675 680 685	
155	aaa cca tac ttc ctg aaa gaa ata ccc atc cag gat gtg gcc att cag	2112
156	Lys Pro Tyr Phe Leu Lys Gly Ile Pro Ile Gln Asp Val Ala Ile Gln	
157	690 695 700	
158	gac ttc act tgt gat gac gga aat gat gac aat agt tgc tcc cca ctt	2160
159	Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu	
160	705 710 715 720	
161	tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt	2208
162	Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys	
163	725 730 735	
164	agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc	2256
165	Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val	
166	740 745 750	
167	aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa	2304
168	Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu	
169	755 760 765	
170	ctc tcc aac tac aaa cat tta aca ctt ata gac tta agt aac aac aga	2352
171	Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg	
172	770 775 780	
173	ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc	2400
174	Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu	
175	785 790 795 800	
176	acc tta att ctt agt tac aac cgt ctg aga tgt att cct cct cgc acc	2448
177	Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr	
178	805 810 815	
179	ttt gat gga tta aag tct ctt cga tta ctt tct cta cat gga aat gac	2496
180	Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp	
181	820 825 830	
182	att tct gtt gtg cct gaagggt gct ttc aat gat ctt tct gca tta tca	2544
183	Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser	
184	835 840 845	
185	cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag	2592
186	His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln	
187	850 855 860	
188	tgg tta tcc gac tgg gtg aag tcg gaa tat aag gag cct gga att gct	2640
189	Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala	
190	865 870 875 880	
191	cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act	2688
192	Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr	
193	885 890 895	
194	ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta	2736
195	Pro Ser Lys Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu	

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196		900		905		910		
197	gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca							2784
198	Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr							
199		915		920		925		
200	tgt aat agt gat cca gtt gac ttt tac cga tgc acc tgt cca tat ggt							2832
201	Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly							
202		930		935		940		
203	ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac							2880
204	Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn							
205		945		950		955		960
206	cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat							2928
207	Pro Cys Lys His Gly Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp							
208		965		970		975		
209	gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa							2976
210	Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu							
211		980		985		990		
212	gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca							3024
213	Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr							
214		995		1000		1005		
215	tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat							3072
216	Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr							
217		1010		1015		1020		
218	aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg							3120
219	Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu							
220		1025		1030		1035		1040
221	aac ccc tgc cag cac gat tca aag tgc atc cta act cca aag gga ttc							3168
222	Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe							
223		1045		1050		1055		
224	aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat							3216
225	Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp							
226		1060		1065		1070		
227	ttt gac gac tgc caa gac aac aag tgt aaa aac gga gcc cac tgc aca							3264
228	Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr							
229		1075		1080		1085		
230	gat gca gtg aac ggc tat acg tgc ata tgc ccc gaa ggt tac agt ggc							3312
231	Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly							
232		1090		1095		1100		
233	ttg ttc tgt gag ttt tct cca ccc atg gtc ctc cct cgt acc agc ccc							3360
234	Leu Phe Cys Glu Phe Ser Pro Pro Met Val Leu Pro Arg Thr Ser Pro							
235		1105		1110		1115		1120
236	tgt gat aat ttt gat tgt cag aat gga gct cag tgt atc gtc aga ata							3408
237	Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile							
238		1125		1130		1135		
239	aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt							3456
240	Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys							
241		1140		1145		1150		
242	gaa aaa ttg gtt agt gtg aat ttt ata aac aaa gag tct tat ctt cag							3504
243	Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln							
244		1155		1160		1165		

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:583 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1845 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19